



## SEQUENCE LISTING

<110> Amatani, Takuya  
Tezuka, Katsunari

<120> CELL SURFACE MOLECULE MEDIATING CELL  
ADHESION AND SIGNAL TRANSMISSION

<130> 06501-039001

<140> US 09/383,551

<141> 1999-08-26

<150> PCT/JP98/00837

<151> 1998-02-27

<150> JAPAN 09-62290

<151> 1997-02-27

<150> JAPAN 10-62217

<151> 1998-02-26

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 600

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(597)

<400> 1

atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa	48
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys	
1 5 10 15	

gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata	96
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	
20 25 30	

ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc	144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	
35 40 45	

cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat	192
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	
50 55 60	

ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg	240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
65 70 75 80	

aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta	288
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
85 90 95	
tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca	336
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser	
100 105 110	
att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg	384
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu	
115 120 125	
cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc	432
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro	
130 135 140	
ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt	480
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu	
145 150 155 160	
att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct	528
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro	
165 170 175	
aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct	576
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser	
180 185 190	
aga ctc aca gat gtg acc cta taa	600
Arg Leu Thr Asp Val Thr Leu	
195	

<210> 2  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys	
1 5 10 15	
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	
20 25 30	
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	
35 40 45	
Gln Gln Phe Lys Met Gln Leu Lys Gly Gly Gln Ile Leu Cys Asp	
50 55 60	
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	
65 70 75 80	
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
85 90 95	
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser	
100 105 110	
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu	
115 120 125	
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro	
130 135 140	

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu  
 145 150 155 160  
 Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro  
 165 170 175  
 Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser  
 180 185 190  
 Arg Leu Thr Asp Val Thr Leu  
 195

<210> 3  
 <211> 2610  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (26)...(622)

<400> 3  
 ggactgttaa ctgtttctgg caaac atg aag tca ggc ctc tgg tat ttc ttt 52  
 Met Lys Ser Gly Leu Trp Tyr Phe Phe  
 1 5  
 ctc ttc tgc ttg cgc att aaa gtt tta aca gga gaa atc aat ggt tct 100  
 Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser  
 10 15 20 25  
 gcc aat tat gag atg ttt ata ttt cac aac gga ggt gta caa att tta 148  
 Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu  
 30 35 40  
 tgc aaa tat cct gac att gtc cag caa ttt aaa atg cag ttg ctg aaa 196  
 Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys  
 45 50 55  
 ggg ggg caa ata ctc tgc gat ctc act aag aca aaa gga agt gga aac 244  
 Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn  
 60 65 70  
 aca gtg tcc att aag agt ctg aaa ttc tgc cat tct cag tta tcc aac 292  
 Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn  
 75 80 85  
 aac agt gtc tct ttt ttt cta tac aac ttg gac cat tct cat gcc aac 340  
 Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn  
 90 95 100 105  
 tat tac ttc tgc aac cta tca att ttt gat cct cct cct ttt aaa gta 388  
 Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val  
 110 115 120  
 act ctt aca gga gga tat ttg cat att tat gaa tca caa ctt tgt tgc 436  
 Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys  
 125 130 135  
 cag ctg aag ttc tgg tta ccc ata gga tgt gca gcc ttt gtt gta gtc 484  
 Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val

140	145	150	
tgc att ttg gga tgc ata ctt att tgt tgg ctt	aca aaa aag aag tat	532	
Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu	Thr Lys Lys Lys Tyr		
155	160	165	
tca tcc agt gtg cac gac cct aac ggt gaa tac atg ttc atg aga gca	580		
Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala			
170	175	180	185
gtg aac aca gcc aaa aaa tct aga ctc aca gat gtg acc cta	622		
Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp Val Thr Leu			
190	195		
taatatggaa ctctggcacc caggcatgaa gcacgttggc cagttttcct caacttgaag	682		
tgcaagattc tcttatttcc gggaccacgg agagtctgac ttaactacat acatcttctg	742		
ctgggtgtttt gttcaatctg gaagaatgac tgtatcagtc aatgggggatt ttaacagact	802		
gccttgggtac tgccgagtc tctcaaaaaca aacaccctct tgcaaccagc tttggagaaa	862		
gcccagctcc tgtgtgtctca ctgggagtggt aatccctgtc tccacatctg ctccatagcag	922		
tgcacagcc agtaaaaaca acacatttac aagaaaaatg ttttaaagat gccaggggta	982		
ctgaatctgc aaagcaaatg agcagccaag gaccagcatc tgtccgcatt tcaactatcat	1042		
actacctctt ctttctgtag ggrtgagaat tcctctttta atcagtcaag ggagatgctt	1102		
caaagctggr gctattttat ttctgagatg ttgatgtgaa ctgtacatta gtacatactc	1162		
agtactctcc ttcaattgct gaaccccagt tgaccatttt accaagactt tagatgcttt	1222		
cttgtgccct caattttctt tttaaaaata cttctacatg actgcttgac agcccaacag	1282		
ccactctcaa tagagagcta tgtcttacat tctttcctct gctgctcaat agttttatat	1342		
atctatgcat acatatatac acacatatgt atataaaaatt cataatgaat atatttgcct	1402		
atatttctccc tacaagaata tttttgctcc agaaagacat gttcttttct caaattcagt	1462		
taaaatgggt tactttgttc aagttagtggt taggaaacat tgcccgggaat tgaaagcaaa	1522		
tttawtttat tatcctattt tctaccatta tctatgtttt catggtgcta ttaattacaa	1582		
gtttagttct tttttagat catattaaaa ttgcaaaaca aatcatcttt aatgggccag	1642		
cattctcatg gggtagagca gaatattcat ttagcctgaa agctgcagtt actatagggt	1702		
gctgtcagac tatacccatg gtgcctctgg gcttgacagg tcaaaatggt ccccatcagc	1762		
ctggagcagc cctccagacc tgggtggaat tccaggggtg agagactccc ctgagccaga	1822		
ggccactagg tattcttgct cccagaggct gaagtacccc tgggaatcac agtggctctac	1882		
ctgcattcat aattccagga tctgtgaaga gcacatatgt gtcagggcac aattccctct	1942		
cataaaaacc acacagcctg gaaattggcc ctggcccttc aagatagcct tctttagaat	2002		
atgatttggc tagaaagatt cttaaataat tggaatatga ttattcttag ctggaatatt	2062		
ttctctactt cctgtctgca tgcccaaggc ttctgaagca gccaatgtcg atgcaacaac	2122		
atttgaact ttaggtaaac tgggattatg ttgtagtta acattttgta actgtgtgct	2182		
tatagtttac aagttagacc cgatatgtca ttatgcatac ttatattatc ttaagcatgt	2242		
gtaatgctgg atgtgtacag tacagtacwt aacttgtaat ttgaatctag tatgggtgtc	2302		
tgttttcagc tgacttgagc aacctgactg gctttgcaca ggtgttcctt gagttgtttg	2362		
cagggtttctg tgtgtgggtt ggggtatggg gaggagaacc ttcatgggtg cccacctggc	2422		
ctggttgtcc aagctgtgcc tcgacacatc ctcatcccaa gcatgggaca cctcaagatg	2482		
aataataatt cacaaaattt ctgtgaaatc aaatccagtt ttaagaggag ccacttatca	2542		
aagagatttt aacagtagta agaaggcaaa gaataaacat ttgatattca gcaactgaaa	2602		
aaaaaaaa	2610		

&lt;210&gt; 4

&lt;211&gt; 2072

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (35) ... (634)

&lt;400&gt; 4

ctggagggga agagtgcagc tgttcctggc agac atg aag ccc tac ttc tcg tgc 55  
Met Lys Pro Tyr Phe Ser Cys  
1 5

gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat 103  
Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn  
10 15 20

gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151  
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln  
25 30 35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199  
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu  
40 45 50 55

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247  
Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser  
60 65 70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295  
Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu  
75 80 85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343  
Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln  
90 95 100

ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt 391  
Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe  
105 110 115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439  
Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln  
120 125 130 135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487  
Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe  
140 145 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535  
Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys  
155 160 165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583  
Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe  
170 175 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc 631  
Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr  
185 190 195

tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct 684  
Ser  
200

```

gaaacttgaa tggagaaagt cttctatatt ctggaccaca gggcatctga cttgattaac 744
tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcactcggaa 804
tttcagcaga ctgccctggg tttgctgagt ccttttaagg caaaccctt cttatagaag 864
accoggctca tatgtattca acaaacagac ctcaactggga tacaatcccc tctttctgcg 924
cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa 984
tgccagggtg tgaatctgta aagtacacag gcagccattg accaccgtct gtcctcgttt 1044
tttcagattc tatttttttc catagagatc agcattcctt ctagaatcag acagtagagg 1104
gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt 1164
accaccatgt tctctaacia cttctatatt ccagctgac actgcttcag ggcttagatg 1224
cctgcttttg ccttcaagtc tccccttaaa gatactcca caggtctact tgggtggcctg 1284
cagccactct gaataggaag tttggtctac aatttcccc ctctgctgct caaaaaaaaa 1344
aattagtaga tatgattttc ccatattctc cctgccaaag taattttttc cagcaaagac 1404
atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa catttctcag 1464
aatcaaaagc aaattaattt tgcggtggtg tttttctacc attatcttgg gtttccatgg 1524
tgctattact cacaagttta gctatttttt tatgcatcat attaaagtgt caagcaagca 1584
gagcaaccct cggttaatgg gcaaacattc tcctggggta gaatgaattg tctatttagc 1644
ccgaaaactg cagtttctgt ggggtggctgc cagactacag ccgtgctttg ctctggcttt 1704
gacagggttg aatagycctc atgascstgg aacagwactc cagactgtgc tggagtccca 1764
aagttaggag ggccatggag cctgggacag gctgctgctt tggctcttag gatctaggaa 1824
raattacaga ggggccaaga cagagttccc tcccctagaa actgtgcagc ctggaagtca 1884
gccctggcac tttaagatag ccttctttag aacatgagtt agttggtagt attctgacgt 1944
gtaaacagcc tatkgittgt cggagctgga ccattttctc cacttccctg tctgcatgcc 2004
taagacttct agagcagcca acgtatatgc aacattaaag aaaaaaaaaa aaaaaaaaaa 2064
aaaaaaaaa 2072

```

<210> 5

<211> 603

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(600)

<400> 5

```

atg aag ccg tac ttc tgc cat gtc ttt gtc ttc tgc ttc cta atc aga 48
Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
1 5 10 15

```

```

ctt tta aca gga gaa atc aat ggc tgc gcc gat cat agg atg ttt tca 96
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30

```

```

ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

```

```

cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

```

```

ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

```

```

atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288

```

Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu		
				85					90						95		
aac	aac	cca	gac	agc	tcc	cag	gga	agc	tat	tac	ttc	tgc	agc	ctg	tcc		336
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser		
			100					105					110				
att	ttt	gac	cca	cct	cct	ttt	caa	gaa	agg	aac	ctt	agt	gga	gga	tat		384
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr		
		115					120					125					
ttg	cat	att	tat	gaa	tcc	cag	ctc	tgc	tgc	cag	ctg	aag	ctc	tgg	cta		432
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu		
	130					135					140						
ccc	gta	ggg	ttg	cca	gct	ttc	gtt	gtg	gta	ctc	ctt	ttt	gga	tgc	ata		480
Pro	Val	Gly	Leu	Pro	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile		
145					150				155						160		
ctt	atc	atc	tgg	ttt	tca	aaa	aag	aaa	tac	gga	tcc	agt	gtg	cat	gac		528
Leu	Ile	Ile	Trp	Phe	Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp		
				165					170					175			
cct	aat	agt	gaa	tac	atg	ttc	atg	gcg	gca	gtc	aac	aca	aac	aaa	aag		576
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys		
			180					185				190					
tct	aga	ctt	gca	ggt	gtg	acc	tca	taa									603
Ser	Arg	Leu	Ala	Gly	Val	Thr	Ser										
		195				200											
<210> 6																	
<211> 836																	
<212> DNA																	
<213> Rattus norvegicus																	
<220>																	
<221> CDS																	
<222> (35)...(682)																	
<400> 6																	
ctggagggga	agagtgcagc	tggtcctggc	agac	atg	aag	ccc	tac	ttc	tcg	tgc							55
	Met	Lys	Pro	Tyr	Phe	Ser	Cys										
		1			5												
gtc	ttt	gtc	ttc	tgc	ttc	cta	atc	aaa	ctt	tta	aca	gga	gaa	ctc	aat		103
Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Asn		
		10				15					20						
gac	ttg	gcc	aat	cac	agg	atg	ttt	tcg	ttt	cac	gat	gga	ggt	gta	cag		151
Asp	Leu	Ala	Asn	His	Arg	Met	Phe	Ser	Phe	His	Asp	Gly	Gly	Val	Gln		
	25				30				35								
att	tct	tgt	aac	tac	cct	gag	act	gtc	cag	cag	tta	aaa	atg	cag	ttg		199
Ile	Ser	Cys	Asn	Tyr	Pro	Glu	Thr	Val	Gln	Gln	Leu	Lys	Met	Gln	Leu		
	40				45				50					55			

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247  
 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser  
                     60                    65                    70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295  
 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu  
                     75                    80                    85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343  
 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln  
                     90                    95                    100

ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt 391  
 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe  
                     105                    110                    115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439  
 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln  
                     120                    125                    130                    135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487  
 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe  
                     140                    145                    150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535  
 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys  
                     155                    160                    165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583  
 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe  
                     170                    175                    180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt aca gca 631  
 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala  
                     185                    190                    195

ccc ctt agg gct ttg ggg aga gga gaa cac tct tca tgt caa gac cgg 679  
 Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg  
                     200                    205                    210                    215

aat taatttggtt atttctattt taaaagaaag acattttttc ccctaaagat 732  
 Asn

aatttttgta tttttatgtg aaagtctgaa tcttcatttt aactcgactt atatactctg 792  
 tgggtatatta aaaataatgt ttgtgaaaaa aaaaaaaaaa aaaa 836

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 7



ctgctcgaga tgaagcccta cttctcg

27

<210> 8

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 8

accctacggg taacggatcc ttcagctggc aa

32

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 9

taactgtttc tcgagaacat gaagtcaggc

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 10

atcctatggg taacggatcc ttcagctggc

30

<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 11

cgtgatattg ctgaagagct tggcggcgaa tgggc

35

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 12

cattcaagtt tcagggaact agtccatgcg ttcc

34

<210> 13  
 <211> 200  
 <212> PRT  
 <213> Rattus norvegicus

<400> 13

Met	Lys	Pro	Tyr	Phe	Ser	Cys	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Lys
1				5					10					15	
Leu	Leu	Thr	Gly	Glu	Leu	Asn	Asp	Leu	Ala	Asn	His	Arg	Met	Phe	Ser
			20					25					30		
Phe	His	Asp	Gly	Gly	Val	Gln	Ile	Ser	Cys	Asn	Tyr	Pro	Glu	Thr	Val
		35				40					45				
Gln	Gln	Leu	Lys	Met	Gln	Leu	Phe	Lys	Asp	Arg	Glu	Val	Leu	Cys	Asp
	50					55					60				
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Thr	Val	Ser	Ile	Lys	Asn	Pro
65					70					75				80	
Met	Ser	Cys	Pro	Tyr	Gln	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
				85					90					95	
Asp	Asn	Ala	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Phe	Leu	Cys	Ser	Leu	Ser
			100					105					110		
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Lys	Asn	Leu	Ser	Gly	Gly	Tyr
		115					120					125			
Leu	Leu	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu
	130					135					140				
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Ala	Ala	Leu	Phe	Gly	Cys	Ile	
145					150					155				160	
Phe	Ile	Val	Trp	Phe	Ala	Lys	Lys	Lys	Tyr	Arg	Ser	Ser	Val	His	Asp
				165					170					175	
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys
			180					185					190		
Ser	Arg	Leu	Ala	Gly	Met	Thr	Ser								
		195					200								

<210> 14  
 <211> 200  
 <212> PRT  
 <213> Mus musculus

<400> 14

Met	Lys	Pro	Tyr	Phe	Cys	His	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Arg
1				5					10					15	
Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser
			20					25					30		
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val
		35				40					45				
Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu
	50					55					60				
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro
65					70					75				80	
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu
				85					90					95	
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser
			100					105					110		
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr
		115					120					125			
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu
	130					135					140				

Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
 145 150 155 160  
 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp  
 165 170 175  
 Pro Asn Ser Glu Tyr Met Phe Met Ala Val Asn Thr Asn Lys Lys  
 180 185 190  
 Ser Arg Leu Ala Gly Val Thr Ser  
 195 200

<210> 15  
 <211> 216  
 <212> PRT  
 <213> Rattus norvegicus

<400> 15  
 Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys  
 1 5 10 15  
 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser  
 20 25 30  
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val  
 35 40 45  
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp  
 50 55 60  
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro  
 65 70 75 80  
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 85 90 95  
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser  
 100 105 110  
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr  
 115 120 125  
 Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
 130 135 140  
 Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile  
 145 150 155 160  
 Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp  
 165 170 175  
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
 180 185 190  
 Ser Arg Leu Ala Gly Thr Ala Pro Leu Arg Ala Leu Gly Arg Gly Glu  
 195 200 205  
 His Ser Ser Cys Gln Asp Arg Asn  
 210 215

<210> 16  
 <211> 200  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<221> VARIANT  
 <222> (1)...(200)  
 <223> Xaa = Any Amino Acid

<400> 16

```

Met Lys Pro Tyr Phe Xaa Xaa Val Phe Val Phe Cys Phe Leu Ile Lys
 1          5          10          15
Leu Leu Thr Gly Glu Xaa Asn Xaa Xaa Ala Asn His Arg Met Phe Ser
          20          25          30
Phe His Xaa Gly Gly Val Gln Ile Ser Cys Xaa Tyr Pro Glu Thr Val
          35          40          45
Gln Gln Leu Lys Met Gln Leu Phe Lys Xaa Arg Glu Val Leu Cys Asp
          50          55          60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65          70          75          80
Met Xaa Cys Xaa Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
          85          90          95
Xaa Asn Xaa Asp Ser Ser Gln Gly Ser Tyr Xaa Xaa Cys Ser Leu Ser
          100          105          110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Xaa Asn Leu Ser Gly Gly Tyr
          115          120          125
Leu Xaa Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
          130          135          140
Pro Val Gly Cys Ala Ala Phe Val Xaa Xaa Leu Leu Phe Gly Cys Ile
145          150          155          160
Xaa Ile Xaa Trp Phe Xaa Lys Lys Lys Tyr Xaa Ser Ser Val His Asp
          165          170          175
Pro Asn Ser Glu Tyr Met Phe Met Ala Val Asn Thr Asn Lys Lys
          180          185          190
Ser Arg Leu Ala Gly Xaa Thr Xaa
          195          200

```

<210> 17  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<221> VARIANT  
 <222> (1)...(214)  
 <223> Xaa = Any Amino Acid

```

<400> 17
Met Leu Xaa Leu Xaa Leu Ala Trp Xaa Leu Xaa Leu Phe Xaa Leu Xaa
 1          5          10          15
Ile Xaa Val Xaa Xaa Xaa Xaa Ile Xaa Val Xaa Gln Xaa Xaa Xaa Xaa
          20          25          30
Xaa Ala Xaa Xaa Asn Gly Xaa Xaa Xaa Xaa Cys Lys Tyr Xaa Xaa
          35          40          45
Pro Xaa Xaa Xaa Xaa Glu Phe Arg Xaa Xaa Leu Leu Lys Gly Xaa Asp
          50          55          60
Ser Xaa Val Xaa Xaa Cys Xaa Xaa Xaa Xaa Thr Tyr Xaa Xaa Gly Asn
65          70          75          80
Xaa Val Xaa Xaa Lys Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Leu Ser Asn
          85          90          95
Asn Ser Val Xaa Phe Xaa Leu Gln Asn Leu Xaa Xaa Xaa Xaa Thr Xaa
          100          105          110
Xaa Tyr Phe Cys Lys Xaa Glu Xaa Met Tyr Pro Pro Pro Tyr Xaa Xaa
          115          120          125
Xaa Xaa Xaa Asn Gly Thr Xaa Ile His Val Xaa Xaa Xaa Xaa Leu Cys

```

130		135		140
Pro Xaa Xaa Xaa Phe Xaa Xaa Trp Xaa Leu Xaa Xaa Val Xaa Xaa Xaa				
145		150		160
Leu Xaa Xaa Tyr Ser Xaa Leu Xaa Thr Ala Xaa Ile Xaa Xaa Xaa Xaa				
	165		170	175
Xaa Lys Lys Arg Ser Xaa Leu Xaa Xaa Gly Xaa Tyr Met Xaa Met Xaa				
	180		185	190
Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Lys Xaa Xaa Gln Pro Tyr Xaa Xaa				
	195	200		205
Asp Phe Xaa Xaa Xaa Xaa				
210				

<210> 18  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Tyr Pro Pro Pro Tyr  
 1 5

<210> 19  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Tyr Met Asn Met  
 1

<210> 20  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Tyr Val Lys Met  
 1

<210> 21  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Phe Asp Pro Pro Pro Phe  
 1 5

<210> 22  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Tyr Met Phe Met  
 1

<210> 23  
 <211> 216  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<221> VARIANT  
 <222> (1)...(216)  
 <223> Xaa = Any Amino Acid

<400> 23  
 Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys  
 1 5 10 15  
 Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser  
 20 25 30  
 Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val  
 35 40 45  
 Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp  
 50 55 60  
 Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro  
 65 70 75 80  
 Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 85 90 95  
 Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser  
 100 105 110  
 Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr  
 115 120 125  
 Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
 130 135 140  
 Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile  
 145 150 155 160  
 Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp  
 165 170 175  
 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
 180 185 190  
 Ser Arg Leu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 195 200 205  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 210 215

<210> 24  
 <211> 16  
 <212> PRT  
 <213> Rattus norvegicus

<400> 24  
 Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg Asn  
 1 5 10 15

<210> 25  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

<400> 25

```

Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
1      5      10      15
Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
20      25      30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
35      40      45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
50      55      60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65      70      75      80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
85      90      95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
100     105     110
Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
115     120     125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
130     135     140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145     150     155     160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
165     170     175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
180     185     190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
195     200     205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
210     215     220

```

<210> 26

<211> 223

<212> PRT

<213> Homo sapiens

<400> 26

```

Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
1      5      10      15
Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
20      25      30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
35      40      45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50      55      60
Lys Ala Tyr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65      70      75      80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
85      90      95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100     105     110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115     120     125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
130     135     140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145     150     155     160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165     170     175

```

Tyr	Ser	Phe	Leu	Leu	Thr	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys
			180					185					190		
Arg	Ser	Pro	Leu	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu
		195					200					205			
Pro	Glu	Cys	Glu	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn	
	210					215					220				